REMARKS

Claims were 1-38 were pending in the application. Claims 18-34 have been canceled, without prejudice, as being directed to a non-elected invention. Claims 1-17 and 35-38 have also been canceled, without prejudice. New claims 39-55 have been added. Accordingly, claims 39-55 will be currently pending in the instant application upon entry of this Amendment. For the Examiner's convenience, the pending claims are set forth in Appendix A.

Support for the new claims may be found throughout the specification and claims, as originally filed. In particular, support for new claims 39-55 may be found at page 9, lines 10-24 of the specification. *No new matter has been added.*

Applicants submit herewith a "Version with Markings to Show Changes Made," which indicates the specific amendments made to the specification and the claims.

Any amendments to and/or cancellation of the claims is not to be construed as an acquiescence to any of the rejections set forth in the instant Office Action, and was done solely to expedite prosecution of the application. Applicants hereby reserve the right to pursue the subject matter of the claims as originally filed in this or a separate application(s).

Priority

In paragraph 3 of the instant Office Action, the Examiner states that "[a]cknowledgment is made of applicant's claim for foreign priority based on multiple applications filed in Denmark during period spanning July 8, 1999 through September 3, 1999. It is noted, however, that applicant has not filed a certified copy of any of the pending foreign applications as required by 35 U.S.C. 119(b)."

Applicants respectfully note that the foreign applications to which Applicants claim priority are German applications, rather than Denmark applications. Applicants respectfully submit that Applicants will provide certified copies of all of the German applications to which this application claims priority prior to issuance of the instant application.

Rejection of claims 1-17 and 35-38 Under 35 U.S.C. §112, second paragraph

The Examiner has rejected claims 1-17 and 35-38 under 35 U.S.C. §112, second paragraph, "as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." In particular, the Examiner is of the opinion that

> The claims must stand alone and should not refer to figures or Appendices from the specification. In claim 35, line 4, it is unclear what is meant by "are not or are not". In claim 36, lines 2 and 3, it is unclear what is meant by "wherein the nucleic acid molecule is disrupted.

Applicants respectfully traverse the foregoing rejection. Applicants have canceled claims 1-17 and 35-38, thereby rendering the foregoing rejection moot as it pertains to these claims. Applicants respectfully submit that new claims 39-55 do not refer to figures or Appendices of the application. Accordingly, Applicants respectfully request reconsideration and withdrawal of the instant rejection.

Rejection of claims 1-17 and 35-38 Under 35 U.S.C. §112, first paragraph

The Examiner has rejected claims 1-17 and 35-38 under 35 U.S.C. §112, first paragraph, "as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." In particular, the Examiner is of the opinion that

> The specification and claims do not indicate what distinguishing attributes are concisely shared by the members of the genera comprising an HA protein or a portion thereof, a fine chemical, an alleleic variant, a homologue of at least 50% identity, a heterologous polypeptide, nucleic acid modifications (i.e. compared to those set forth in Appendix A or of SEQ ID NO:1) or a modified regulatory region of a molecule. Nor does the specification describe elements which are essential to various functions of each claimed genus. The specification does not place any limit on the number of nucleic acid or amino acid substitutions, deletions, insertions and/or additions that may be made within each genus. The scope of the claims includes numerous structural variants, and each genus is highly variant because a significant number [of] structural differences between genus members is permitted. Concise structural features that could distinguish compounds from others in each genus are missing from

the disclosure. No common structural attributes identify the members of the various genera.

Applicants respectfully traverse the foregoing rejection. However, in the interest of expediting prosecution and in no way acquiescing to the Examiner's rejection, Applicants have canceled claims 1-17, thus rendering the instant rejection moot as it pertains to these claims. With respect to new claims 39-55, Applicants respectfully submit that there is sufficient written description in Applicants' specification regarding SEQ ID NO:1 and nucleic acid molecules with a significant degree of homology to SEQ ID NO:1, to inform a skilled artisan that Applicants were in possession of the claimed invention at the time the application was filed as required by section 112, first paragraph. (see M.P.E.P. 2163.02). In order to meet the written description requirement of the first paragraph of 35 U.S.C. § 112, it is not necessary that a patent specification describe each and every specific member of a genus recited in a claim.

Applicant's respectfully direct the Examiner's attention to Example 14 of the *Revised Interim Written Description Guidelines Training Materials* which provides that a claim directed to variants of a polypeptide having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity."

Similarly, in the present case, claims 43 and 44 are directed to isolated nucleic acid molecules comprising or consisting of a nucleotide sequence that is at least 90% identical to the nucleotide sequence shown in SEQ ID NO:1, wherein the nucleotide sequence encodes a polypeptide capable of modulating cell wall biosynthesis. Claims 45 and 46 are directed to isolated nucleic acid molecules comprising or consisting of a nucleotide sequence that is at least 90% identical to the nucleotide sequence shown in

SEQ ID NO:1, wherein the nucleotide sequence encodes a polypeptide capable of modulating the production of a fine chemical.

Applicants have disclosed in the instant specification assays for identifying all of the at least 90% identical variants of SEQ ID NO:1, which encode polypeptides capable of modulating cell wall biosynthesis or capable of modulating production of a fine chemical (see, for example, page 48, line 8 through page 49, line 24; page 53, line 33 through page 55, line 30; page 51, line 20 through page 52, line 9; and page 57, line 24 through page 59, line 35 of the specification).

Based on the foregoing teachings in Applicants' specification and the knowledge generally available in the art, one skilled in the art would conclude that Applicants were in possession of the claimed invention at the time of filing of the application. Accordingly, Applicants respectfully request reconsideration and withdrawal of the foregoing rejection under 35 U.S.C. § 112, first paragraph.

Rejection of claims 1-17 and 35-38 Under 35 U.S.C. §112, first paragraph

The Examiner has rejected claims 1-17 and 35-38 under 35 U.S.C. §112, first paragraph, because

> the specification, while being enabling for the construction of genomic libraries of Cornebacterium glutamicum ATCC 13032, and their enabling subcloning into plasmids or cosmids, and their subsequent sequence determination, does not reasonable provide enablement for the production of fine chemicals from any/or all isolated nucleic acids, nor diagnosis or C. Diptheria in a subject, nor the disruption of expression of any and/or all of these nucleic acids, not any and/or all modifications of such nucleic acids, nor a determination of their regulatory regions. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Applicants respectfully traverse the foregoing rejection. However, in the interest of expediting prosecution and in no way acquiescing to the Examiner's rejection, Applicants have canceled claims 1-17, thus rendering the instant rejection moot as it pertains to these claims. With respect to new claims 39-55, it is Applicant's position that

one of ordinary skill in the art would be able to make and use the claimed invention using only routine experimentation.

Applicant's respectfully direct the Examiner's attention to Example 14 of the *Revised Interim Written Description Guidelines Training Materials*, which provides, as set forth above, that a claim directed to variants of a protein having SEQ ID NO:3 "that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A→B" with an accompanying specification that discloses a single species falling within the claimed genus, satisfies the requirements of 35 U.S.C. §112, first paragraph for written description. The rationale behind the foregoing conclusion, as presented by the *Written Description Guidelines*, is that "[t]he single species disclosed is representative of the genus because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which Applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:3 which are capable of the specified catalytic activity." The Guidelines also provide that "***[t]he procedures for making variants of SEQ ID NO:3 are conventional in the art and an assay is described which will identify other proteins having the claimed catalytic activity. Moreover, procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art.***"

As set forth in Example 14 of the Written Description Guidelines, "procedures for making variants of SEQ ID NO:3 which have 95% identity to SEQ ID NO:3 and retain its activity are conventional in the art." Likewise, procedures for making variants of SEQ ID NO:1 of the instant invention which encode polypeptides which retain a specific activity are also conventional in the art. Furthermore, Applicant has disclosed in the instant specification assays for identifying all of the at least 95% identical variants of SEQ ID NO:1 which encode proteins capable of ***modulating cell wall biosynthesis and fine chemical production*** (see, for example, page 48, line 8 through page 49, line 24; page 53, line 33 through page 55, line 30; page 51, line 20 through page 52, line 9; and page 57, line 24 through page 59, line 35 of the specification). Modulation of cell wall biosynthesis and fine chemical production are readily testable by one of skill in the art by

acid molecules comprising or consisting of a nucleotide sequence which is at least ***90% identical to the nucleotide sequence of SEQ ID NO:1***, or a complement thereof, wherein said nucleotide sequence encodes a polypeptide which is capable of modulating the production of a fine chemical.

Kobayashi (GenBank Accession No. AB003132) discloses a 4,116 base pair polynucleotide sequence. The nucleotide sequence of SEQ ID NO:1 of the instant invention comprises 1,581 base pairs. As shown in the alignment provided by the Examiner, the sequences disclosed in Kobayashi is only identical to SEQ ID NO:1 over a small portion of the entire length of the sequence. A sequence alignment of the ***entire length*** of the nucleotide sequence disclosed by Kobayashi with SEQ ID NO:1 of the instant invention would result in a much lower percent identity than the claimed 90% identity. Accordingly, Kobayashi does not teach each and every element of the claimed invention.

Smith *et al.* (SEQ ID NO:30 of USPN 5,871,960) discloses a 2,289 base pair polynucleotide sequence. As shown in the alignment provided by the Examiner, SEQ ID NO:30 is identical to only small fragments, *i.e.*, fragments of no greater than 19 consecutive nucleotides, of SEQ ID NO:1. An alignment of the ***entire length*** of the nucleotide sequence disclosed by Smith *et al.* with the entire length of SEQ ID NO:1 of the instant invention would result in a much lower percent identity than the claimed 90% identity. Accordingly, Smith *et al.* does not teach each and every element of the claimed invention.

Wachi (GenBank Accession No. AB015023) discloses a polynucleotide sequence of 2,291 nucleotides. As shown by a global alignment of the ***entire length*** of the nucleotide sequence disclosed by Wachi and SEQ ID NO:1 of the instant invention (provided herewith as Appendix B), Wachi is only ***68.1% identical*** to SEQ ID NO:1, rather than the 98.5% identity indicated by the local alignment provided by the Examiner. Accordingly, the sequence disclosed by Wachi does not disclose each and every element of the claimed invention. Accordingly, for the reasons set forth above, Applicants respectfully request reconsideration and withdrawal of the instant 35 U.S.C. §102(b) rejection.